

Figure 1

A - AMPHI mid points of blocks.
 R - Residues matching the Rothbard/Taylor motif.
 D - Residues matching the IAd motif.
 d - Residues matching the IEd motif.

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      5   10   15   20   25   30   35   40   45   50   55   60   65   70   75
MDSLASLVLCGVSLLLSGTVEGAMDILILINSLPLVSDAETSLTCIASGWRPHEPITIGRDFEALMNQHQPLeVT
.....AAA.....AAAAA.AAAAAAAAAAAAAAAAAAAAA
.....RRRRRRRR.....RRRRR.....RRR
....DDDDDD.DDDDDD.....DDDDDDDDDD.....DD
.....

      80   85   90   95  100  105  110  115  120  125  130  135  140  145  150
QDVTREWAKKVVKREKASKINGAYFCEGRVGEAIRIRTMKMRQQASFLPATLTMTVDKGDNVNISFKKVLiKE
AAAAAA.....AAA.....RRRR.RRRR.....RRRR.
RRRRRRRRRRRRRR.....RRRR.RRRR.....RRRR.
DDDD.....DDDDDDDD.....DDDDDD.....
.....ddddd.....

     155  160  165  170  175  180  185  190  195  200  205  210  215  220  225
EDAVIYKNGSFIHSVPRHEVPDILEVHLPHAQPODAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCT
.....AAAAAAAAA.....AAAAAAAAA.....AAAA
.....RRRR.....RRRR.RRRR.....RRRR.
.....DDDDDD.....DDDDDD.....
.....

     230  235  240  245  250  255  260  265  270  275  280  285  290  295  300
ACMNGNVCHEDTGECICPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
AAAA.....AAAAAAAAAAAAAAAAAAAAA.....AAA.....AAA.....
.....RRRR.....RRRR.....
.....

     305  310  315  320  325  330  335  340  345  350  355  360  365  370  375
ACHPGFYGPDCKLRCSCNNGEMCDRFQGCCLSPGWQGLQCEREGIPRMTPKIVDLPDHIEVNSGKFNPICKASGW
.AAA.....AAAAAA.....AAAAAAAAAAAAAAAAA.....AAAAA....
....RRRR.....RRRRRRRR.....
.....DDDDDD.....
.....

     380  385  390  395  400  405  410  415  420  425  430  435  440  445  450
PLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSGVWVCSVNTVAGMVEKPFNISVKVLPKPLNA
.....AAAAAA.....AAAA.....AAAAAA.....AAAAAA
.....RRRR.....RRRR.....RRRR.....RRRR.....
.....

     455  460  465  470  475  480  485  490  495  500  505  510  515  520  525
PNVIDTGHNFVAVINISSEPYFGDGPiKSKKLLYKPNHYEAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEG
AAAAAA.....AAAAAAAAAAAAAAAAAAAAA.AA.....
.....RRRR.....RRRR.....RRRR.....
.....

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Figure 1 (cont.)

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530 535 540 545 550 555 560 565 570 575 580 585 590 595 600
GEGHPGPVRRFTTASIGLPPPRGLNLLPKSQTTLNLTWQPIFPSSSEDDFYVEVERRSVQKSDQONIKVPGNLTSTV
.....AAAAAA.....AAAAAA.....AAAAAA
.....RRRR.....RRRR.....
.....DDDD
.....

605 610 615 620 625 630 635 640 645 650 655 660 665 670 675
LLNNLHPREQYVVRARVNTKAQGEWSEDLTAWTSLDILPPQPENIKISNITHSSAVISWTILDGYSISSITIRYK
AAA.....AAAAA.AAAAA.....AA.AAA.....AAAAAA.....
.....
DD.....DDDDDDDDDD.....DDDDDD
.....

680 685 690 695 700 705 710 715 720 725 730 735 740 745 750
VQGNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGSSNPAFSHELVTLPESQAPADLGGGKMLLIA
.....AAAA
.....RRRRR.RRRRR.....RRRR.....
.....DDDDDD
.....

755 760 765 770 775 780 785 790 795 800 805 810 815 820 825
ILGSAGMTCLTVLLAFLIILQLKRANVQRRMAQAFQNVREEPAVQFNSGTLALNRKVKNPDPTIYPVLDWNDIK
.....AAA.....AAAAAAAAA.....AAAA.....A
.....RRRR.....
.....DDDDDD
.....dddd
.....

830 835 840 845 850 855 860 865 870 875 880 885 890 895 900
FQDVIGEGNFGQVLKARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCCKLGHPNIIINLLGACEHRGYLYL
AA.....AAAAA.....AAAAAAAAA.AAAA.AAAA.....AAAAAAAAAAAAAAAAA.....
..RRRR.....RRRRR..RRRR.....RRRR.....
.....DDDDDD
.....dddd.....dddd
.....

905 910 915 920 925 930 935 940 945 950 955 960 965 970 975
AIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARNILVGEN
.....AAAAAAAAAAAAA.....AAA.....AAA.AAAAAAAAAA.....
..RRRRR...RRRR..RRRR.....RRRRRRRR..RRRR.....RRRR.....
.....DDDDDDDDDD
.....dddd
.....

980 985 990 995 1000 1005 1010 1015 1020 1025 1030 1035 1040 1045 1050
YVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSDVWSYGVLLWEIVSLGGTPYCGMTCAELYEK
AAAAA.....AAAAAA.....AAA.....AAAA.....AAAAAA
..RRRR.....RRRRRRRRR.....RRRR.....RRRR.....RRRR.....
.....
.....

1055 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125
LPQGYRLEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEAAA
AAAAAAAAAAAAA.....AAAAAA.....AAAAAA
.....RRRRRRR.....RRRR..RRRR.....
.....DDDDDD
.....

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Potential T cell epitopes:

TEK 1 aa 55-90
TEK 2 aa 163-176
TEK 3 aa 345-362

TEK 4 aa 427-442
TEK 5 aa 530-542

Figure 2

TEK = TIE2

Approx position 1

50

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TEK      MD-SLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIAS--
TIE1     MVWRVPPFLL--PILFLASHVGA AVDLTLLANLRLTDPQRFFLTGVSGEA
          *      . . . . . * . . . . * . . . . * . . . . * . . . . * . . . . *

TEK      -----GWRPHEPITIGRDFEALMNQHODPLEVTQDVTREWAKKVWKR
TIE1     GAGRGSDAWGP--PLLLEKDDRIVRTPPGPPLRLARNGSHQ---VTLRGF
          . * * * . . . . * . . . . . * . . . . . * . . . . . * . . . . . *

TEK      EKASKINGAYFCEGRVRGEAIRIRTMKMRQQASFLPATLTMTVDKGDNVN
TIE1     SKPSDLVGVFSCVGGAGARRTRVIYVHNSPGAHL L PDKVTHTV NKGDTAV
          * . * . * . * . * . * . . . . * . . . . * . . . . * . . . . *

TEK      ISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPD-ILEVHLPHAQPDAGVY
TIE1     LSARVHKEKQTDVIWKSNGSYFYTLDWHEAQDGRFLLQLPNVQPPSSGIY
          . * . . . * . . . . . * . . . . . * . . . . . * . . . . . * . . . . . *

TEK      SARYIGGNLFTSAFTRLIVRCEAQKWGPECNHLCTACMNGVCHEDTGE
TIE1     SATYLEASPLGSAFFRLIVRGCGAGRWGPGCTKECPGCLHGGVCHDHGDE
          ** * . . . . * . . . . * . . . . * . . . . * . . . . * . . . . *

TEK      CICPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCPLDPYGCSC
TIE1     CVCPPGFTGTRCEQACREGRFGQSCQECPGISGCRGLTFCLPDPYGCSC
          * . . . . * . . . . * . . . . * . . . . * . . . . * . . . . *

TEK      ATGWKGLQCNEACHPGFYGPDCCKLRCSNNGEMCDRFGQCLCSPGWQGLQ
TIE1     GSGWRGSQCQEACAPGHFGADCR LQCQCQNGGTCDRFSGCVCPSGWHGVH
          . . . . * . . . . * . . . . * . . . . * . . . . * . . . . * . . . . *

TEK      CEREGIPRMTPKIVDLPDHIEVNSGKFNP I-CKASGWPLPTNEEMTLVKP
TIE1     CEKSD---RIPQILNMASELEFNLETMPRINCAAAGNPPFVRGSIELRKP
          * . . . . * . . . . * . . . . * . . . . * . . . . * . . . . *

TEK      DGTVLHPKDFNHTDHFSAIFTIHRILPPDSGVWVCSVNTVAGMVEKPFN
TIE1     DGTVLLSTKAIVEPEKTTAEFEVPRLVLADSGFWECEVSTSGGQDSRRFK
          * . . . . * . . . . * . . . . * . . . . * . . . . * . . . . *

TEK      ISVKVLPKPLNAPNVIDTGHNF AVINISSEPYFGDGPIKSKLLYKPVNH
TIE1     VNVKVPPVPLAAPRL-LTKQSRQLVVSPLVSFSGDGPISTVRLHYRPQDS
          . . . . * . . . . * . . . . * . . . . * . . . . * . . . . *

TEK      YEAWQHIQVT-NEIVTLNLYLEPRTEYELCVQLVRRGEGEGHPGPVRRFT
TIE1     TMDWSTIVVDPSENVTLMLNLRPKTGYSVRVQLSRPGEGEGAWGPPTLMT
          * . . . . * . . . . * . . . . * . . . . * . . . . * . . . . *

TEK      TASIG-LPPPRGLNLLPKSQTTLNLTWQ-PIFPSS--EDDFYVEVERRSV
TIE1     TDCPEPLLQPWLEGWHVEGTDRLRVSWSLPLVPGPLVGDGFLRLRLWDGTR
          * . . . . * . . . . * . . . . * . . . . * . . . . * . . . . *

TEK      QKSDQONIKVPGNLTSVLLNNLHPREQYVVRARVNTKAQGEWSEDLTAWT
TIE1     GQERRENVSSPQARTA-LLTGLTPGTHYQLDVQLYHCTLLGPASPPAHVL
          . . . . * . . . . * . . . . * . . . . * . . . . * . . . . *

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Figure 2 (cont.)

TEK LSDILPPQPENIKISNITHSSAVISWTILDGYSISSITIRYKVQGNEDQ
TIE1 LPPSGPPAPRHLHAQALSDSEIQLTWKHPEA--LPGPIISKYVVEVQVAGG
* . ** * * * *

TEK HVD---VKIKNATIIQYQLKGLEPETAY-----QVDIFAENNIGSSNPA
TIE1 AGDPLWIDVDRPEETSTIIRGLNASTRYLFRMRASIQGLGDWSNTVEEST
* * *

TEK FSHELVT---LPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQ
TIE1 LGNGLQAEQPVQESRAAEE-GLDQQLILAVVGSVSATCLTILAALLTLVC
* * *

TEK LKRANVQRRMAQAFQNVN-EEPAVQFNSGTLALNRKVKNPDPTIYPVLD
TIE1 IRRSCLHRRRTFTYQSGSGEETILQFSSGTLTLTRPKLQPEPLSYPLVE
* * *

TEK WNDIKFQDVIGEGNFGQVLKARIKKDGLRMDAAIKRMKEYASKDDHRDFA
TIE1 WEDITFEDLIGEGNFGQVIRAMIKKDKLKMNAAIKMLKEYASENDHRDFA
* * *

TEK GELEVLCKLGHPNIINLLGACEHRGYLYLAIEYAPHGNLLDFLRKSRVL
TIE1 GELEVLCKLGHPNIINLLGACKNRGYLYIAIEYAPYGNLLDFLRKSRVL
* * *

TEK ETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARNI
TIE1 ETDPAFAREHGTASTLSSRQLLRFASDAANGMQYLSEKQFIHRDLAARNV
* * *

TEK LVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD
TIE1 LVGENLASKIADFGLSRGEEVYVKKTMGRLPVRWMAIESLNYSVYTTKSD
* * *

TEK VWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPGQYRLEKPLNCDDEVYDL
TIE1 VWSFGVLLWEIVSLGGTPYCGMTCAELYEKLPGQYRMEQPRNCDDEVYEL
* * *

TEK MRQCWREKPYERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSA
TIE1 MRQCWRDRPYERPPFAQIALQLGRMLEARKAYVNMSLFENFTYAGIDATA
* * *

TEK EEAA
TIE1 EEA-

Potential epitopes as located on Fig. 1 (same numbering system used)

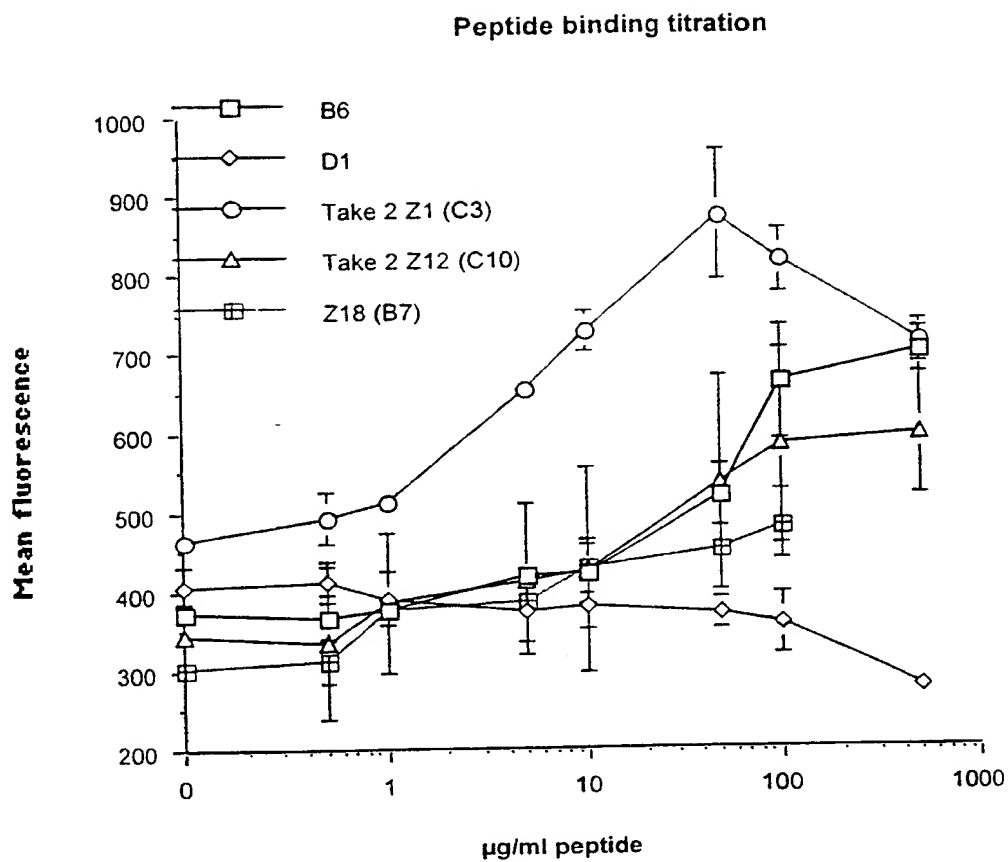
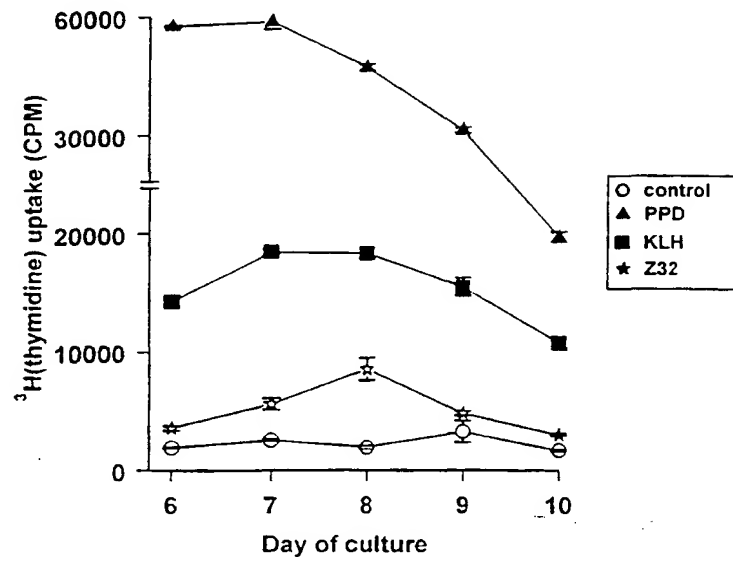


Figure 3

T cell proliferation responses of volunteer 1

a) non enriched cells



b) CD45RA+ Enriched cells

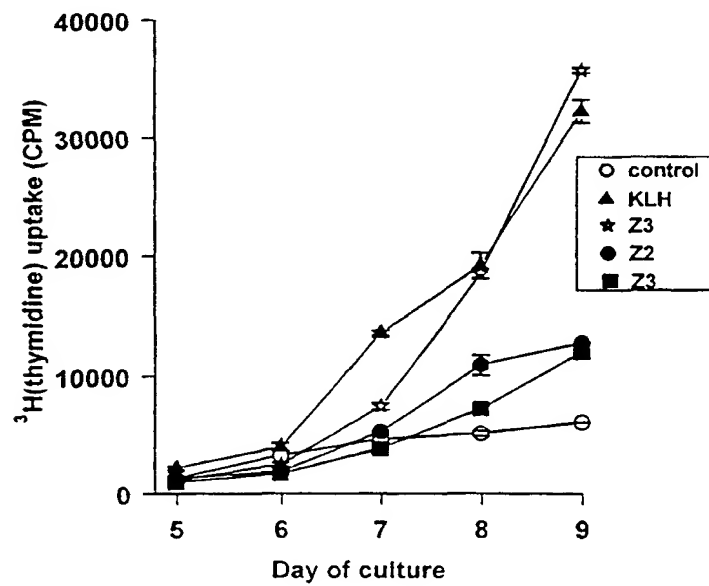


Figure 4

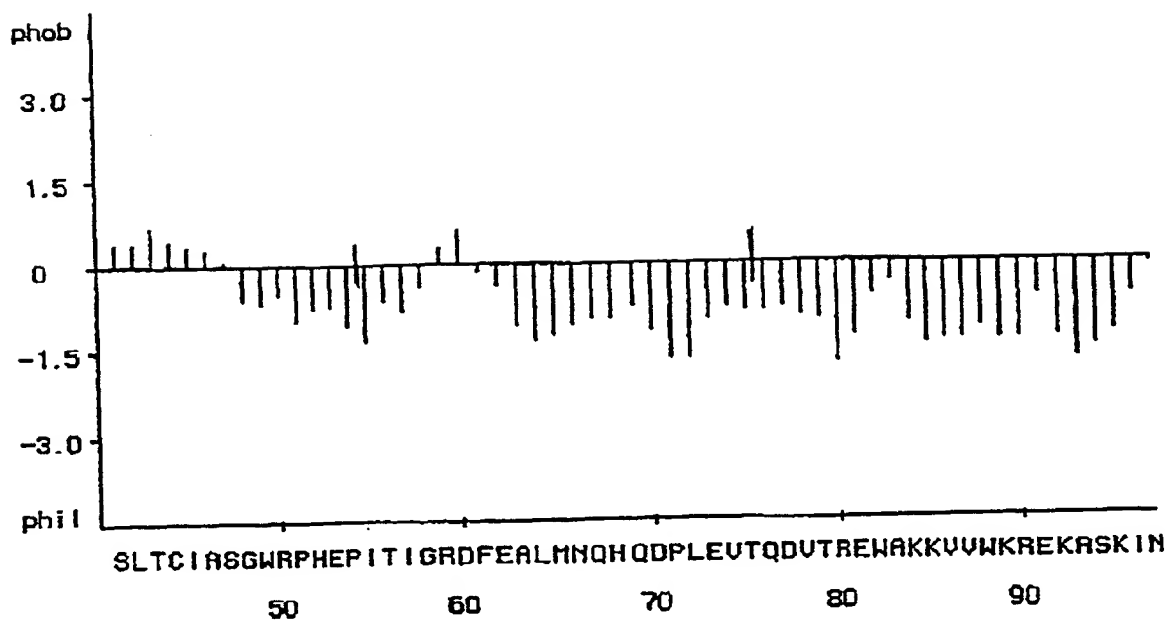


Figure 5